

1 / 9

1	Nor (1rom)	-----	-----	-----	masga	sfpfsrasgp	(16)
2	Ery F (1oxa)	-----	-----	-----	atv	dle-sdsfhv	(13)
3	Terp (1cpt)	-----	-----	mda	ratipehiar	tvilpqgyad	(23)
4	Cam (3cpp)	-----	tteti	snanlaplp	hvpelvfdf	dmynpsnl	(36)
5	BM3 (2hpd)	-----	-----	t	ikempqpkf	gelknplln	(21)
6	2C5 (1dt6)	-----	-----	makkt	sskgklp	tffgiigni	(25)
7	CPC5_RABIT	mdpv	vvlvlgcl	lllsiwkqns	grgkl-p	tffgiigni	(43)
8	cyp51 (1e9x)	-----	-----	ms	avalprvs	hdehghleef	(22)
9	CP31_RAT	dllsaltlet	wlllavvlvl	lygfgtrthg	lfkkqgi	kellffgtvl	
10	CP33_HUMAN	alipdlamet	wlllavslvl	lylygthshg	lfkklgi	tlflflgni	
11	CP34_HUMAN	alipdlamet	wlllavslvl	lylygthshg	lfkklgi	tlflflgni	(50)
12	CP35_HUMAN	mdlipnlavet	wlllavslvl	lylygtrthg	lfkrlgi	tlflflgnvl	
13	C343_HUMAN	mdlipnfamet	wllvatsvl	lyiygthshk	lfkklgi	tlflflgti	
14	CP36_RABIT	mdli--fslet	wlllaasvl	lylygtsthg	lfkkmgi	tlflfigti	
15	CP37_HUMAN	mdlipnlavet	wlllavslvl	lylygtrthg	lfkklgi	tlflflgni	(51)
16	CP3C_CANFA	mdlipsfstet	wlllaisvl	lylygtythg	ifrkligi	tlflfvgti	
17	CP3T_FIG	mdlipgfstet	wlllatsvl	lylygtysg	lfkklgi	tlflfygni	
18	CP3D_MOUSE	mdlipnfsmet	wlllatsvl	lylygthshg	lfkklgi	kellflgti	

1	e---pp	AEFA	KLRA	-----	n	PVSQVKLE	dg	SLAWLVTKHK	DVCFV	atse-	(58)
2	d----	WYST	YAEI	ret--	a	EVTPVREL	-g	QDAWLVTGYD	EAKAA	alsdl-	(54)
3	d-ev---	LYPA	FKWL	rde--	q	PLAMAHTE	gy	QPMWIATKHA	DVMQI	gkqpg	(68)
4	g-----	VOEA	WAVL	qesnvp		DLVWTRCN	-g	GHWTATRCQ	LIREA	yedyr	(79)
5	t-d-k-	EVOA	LMKL	adel-g		ELFKTEAE	-g	RVTRYLSSOR	LIKEAC	-des	(67)
6	qidakd	ISKS	LTKF	seg--	g	PVFTVYLG	mk	STVVLHGYE	AVKEA	vdlg	(73)
7	qidakd	ISKS	LTKF	seg--	g	PVFTVYLG	mk	STVVLHGYE	AVKEA	vdlg	(91)
8	r-t-d-	PIGL	MORV	rdec-g		DVGTFOLA	-g	KOVVLLSGSH	ANEFF	-rag	(66)
9	nyy-mg	LWKF	DVECH	kkkg-		KIWGLFDG	qm	ELFAITDTE	MIKNV	lvkec	
10	syh-kg	FCMF	DMECH	kkkg-		KVWGFYDG	qq	VLAITDPD	MIKLV	lvkec	
11	syh-kg	FCMF	DMECH	kkkg-		KVWGFYDG	qq	VLAITDPD	MIKTV	lvkec	(97)
12	syr-qg	LWKF	DTECY	kkkg-		KMWGTYEG	ql	VLAITDPD	VIRTV	lvkec	
13	fyl-rg	LWNF	DRECN	ekkg-		EMWGLYEG	qq	MLVIMDPD	MIKTV	lvkec	
14	eyr-kg	IWDF	DIECR	kkkg-		KMWGLFDG	rq	LMVITDPD	MIKTV	lvkec	
15	sfr-kg	YWTF	DMECY	kkkg-		KVWGIYDC	qq	MLAITDPD	MIKTV	lvkec	(98)
16	gyr-ng	FYVF	DMKCF	skkg-		KMWGFYDG	rq	VLAITDPD	MIKTV	lvkec	
17	gyr-kg	VDHF	DKKCF	qqg-		KMWGVYDG	rq	LLAVTDPN	MIKSV	lvkec	
18	ayq-kg	FWEC	DIQCH	kkkg-		KMWGLYDG	rq	VLAITDPD	IIKTV	lvkec	

CSB 1*

CSB 1**

CSB 1

1	klskvr----	trqgfpel	---	SASGKQa	a-----	ka	-kp	TFVDMDE	(91)
2	rlssdpkkky	pgvevefpay	lgf	PEDVRN	-----	y	fat	NMGTSDP	(94)
3	lfsnae----	gse	ily	DONNEAF	mrsisggcph		vid	SLTSMDE	(107)
4	hfsse----	cpfi--	---	PREAGE	-----	a	ydf	IFTSMDE	(105)
5	rfdknl----	-----	---	SOALKEFv	r-----	df	agd	GLFTSWT	(91)
6	eefagr----	-----	---	gSVEILEk	vs-----		kgl	GIAFSNA	(98)
7	eefagt----	-----	---	gSVEILEk	vs-----		kgl	GIAFSNA	(117)
8	ddlddq----	-----	---	AKAYPFm	t-----	pi	fge	GVVEDAS	(92)
9	fsvftn----	-----	---	RRDFGPv	gi-----		mgk	AVSVAKD	
10	ysvftn----	-----	---	REFPGPv	gf-----		mks	AIISIAED	
11	ysvftn----	-----	---	REFPGPv	gf-----		mks	AIISIAED	(122)
12	ysvftn----	-----	---	RRSLGPv	gf-----		mks	AIISIAED	
13	ysvftn----	-----	---	QMPLGPm	gf-----		lks	ALSFAED	
14	ysvftn----	-----	---	RRSFGPv	gf-----		mkk	AVSISED	
15	ysvftn----	-----	---	RRPFGPv	gf-----		mkn	AIISIAED	(123)
16	ysvftn----	-----	---	RRTLGPv	gf-----		mks	AIISLED	
17	ysvftn----	-----	---	RRSFGPl	ga-----		mrn	ALSIAED	
18	ystftn----	-----	---	RRRFGPv	gi-----		lkk	AIISISEN	

CSB 2A*

CSB 2A**

2 / 9

1	--PEHMHORS MVEPTftpea vk--nPOBYL ORTVDDLLEQ MKOKgcangp	(137)
2	--PTHTRLRK LVSQEEtvrr -----VEAMRPRVEQITAEI LDEVgds-gv	(136)
3	--PTHAYRG LTLNWqpas ir--kleENTRRLAQASVOR LLDF-d--ge	(150)
4	--PEORQFRA LANOVVgmpv vd--kleNRI OELACSLIES LRPO----gq	(147)
5	hekNNKKAHN ILPSFsqqm m--gYHAMMEVDIAVQAVQK WERLn-adeh	(138)
6	--KTNKEMRR FSLMTLnfg mglrsIEDRI QEEARCVVEE LRKTN--asp	(145)
7	--KTNKEMRR FSLMTLnfg mglrsIEDRI QEEARCVVEE LRKTN--asp	(163)
8	--PERREMLHNAALRgeq -----MKGHAATIEDOVRRM IADWg-eage	(133)
9	--EEEMRYFA LLSPTftsg-rl--eMFPII EQYGDIVVKY LKQEAetgkp	
10	--EEEMRLRS LLSPTftsg-kl--eMVPII AQYGDVVRN LRREretgkp	
11	--EEEMRLRS LLSPTftsg-kl--eMVPII AQYGDVVRN LRREaetgkp	(168)
12	--EEEMRLRS LLSPTftsg-kl--eMFPII AQYGDVVRN LRREaekgkp	
13	--EEEMRIET LLSPAftsv-kl--eMVPII SQCGDMVRS LRQEAensks	
14	--EDMERVET LLSPTftsg-kl--eMLPII AQYGDVVRN LRQEAekgkp	
15	--EEEMRLRS LLSPTftsg-kl--eMVPII AQYGDVVRN LRREaetgkp	(169)
16	--EEEMRMET LLSPTfttg-kl--eMFPII GQYGDVVRN LRKEaekgka	
17	--EEEMRIET LLSPTftsg-kl--eMFPII SHYGDLVSN LRKEaekgkp	
18	--EEEMRIET LLSPTftsg-rl--eMFPII NQFTDVVRN MRQGLgegkp	

CSB 2A

CSB 2B

1	VDLVREFALP VPSYBYTEL GVP-----	FNDELYL TOONAIRtng	(177)
2	VDIVDRFAHP LPIKVCELL GVD-----	EAARGAY GRWSSEILvm	(176)
3	CDPMTOCALY YPLHVMTAL GVP-----	EDDEPIM LKLTODFgv	(190)
4	CNETDYAEP FPIRMMLLA GLP-----	EEDIPHL KYLTDOMtrp	(187)
5	IEVPEDMTRL TLDITGLCG NYRfnsfyrd	qphFFITSMV RALDEAMNkl	(188)
6	CDPTFILGCA PCNVICSVI HNRfdyk--d	EEFLKLM ESLHENVEll	(190)
7	CDPTFILGCA PCNVICSVI HNRfdyk--d	EEFLKLM ESLNENVRil	(208)
8	IDLLDFFAEL TIYTSSACLI GKRF-----rd	qldGRFAKLY HELERGTDpl	(179)
9	VTMKKVFAY SMDVITSTS GVNvds1--n	NPKDPFV ETKKLLRfd	
10	VTLKDVFGAY SMDVITSSS GVNvds1--n	NPQDPLV ENTKKLLRfd	
11	VTLKDVFGAY SMDVITSTS GVNids1--n	NPQDPFV ENTKKLLRfd	(213)
12	VTLKDIFGAY SMDVITGTS GVNids1--n	NPQDPFV ESTKKFLKfg	
13	INLKDFGAY TMDVITGTL GVNids1--n	NPQDPFL KNMKLLKld	
14	VDLKEIFGAY SMDVITGTS GVNids1--r	NPQDPFV KNVRRLLKfs	
15	VTLKHVFAY SMDVITSTS GVSids1--n	NPQDPFV ENTKKLLRfn	(214)
16	INLKDVFGAY SMDVITSTS GVNids1--n	HPQDPFV ENTKKLLKfd	
17	VTMKDIFGAY SMDVITSTA GVNids1--n	NPQDPFV ENSKKLLKfs	
18	TSMKDIFGAY SMDVITATS GVNids1--n	NPQDPFV EKIKKLLKfd	

CSB 3

CSB 4

1	-----s stareASAAN OELDYLAII VEORLV----	(204)
2	d-----p eraeqRQAA REVVNFILDL VERRRT----	(204)
3	-----eaarrFHETI ATEYDYNGF TVDRRS----	(216)
4	d-----g sm--tFAEAK EALYDYLIPI IEORRQ----	(213)
5	qra---npdd -pa---y--d enkrqFOEDI KVMNDLVDKI IADRKAs---	(226)
6	gtpwlqvynn fpalldyfp- gihktLLKNA DYIKNFIMEK VKEHOKl--ld	(238)
7	sspwlvqvynn fpalldyfp- gihktLLKNA DYIKNFIMEK VKEHEKl--ld	(256)
8	ayv---dpvl -pi-----esfrrRDEAR NGLVALVADI MNGRIAnp--	(216)
9	ffd--plfls vvlfpfltpi yemlnICMFP KDSIEFFKKF VYRMKEtrld	
10	fld--pffls itvfpflipi levlnICVFP REVTFNLRKA VKRMKESrle	
11	fld--pffls itvfpflipi levlnICVFP REVTFNLRKS VKRMKESrle	(261)
12	fld--plfls iilfpfltpv fealnVSLFP KDTINFLSKS VNRMKKsrln	
13	fld--pfl1l islfpfltpv fealnIGLFP KDVTFLKNS IERMKESrlk	
14	ffd--pllls itlfpfltpv fealhISMFP KDVMDFLKTS VEKIKDdr1k	
15	p1d--pfvls ikvfpfltpi lealnITVFP RKVISFLTKS VKQIKEgrlk	(262)
16	fld--pfffs iilfpfltpv feilnIWLF KKVTDFFRKS VERMKEsr1k	
17	ffd--pfl1s liifpfltpi fevlnITLFP KSSVNFFTKS VKRMKESr1t	
18	ifd--plfls vtlfpfltpv fdalnVSLFP RDVISFFTKS VERMKENzm1k	

CSB 5

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1	---	epkd	DI	SKLCTeqv	kp	--g-----	ni	DKSDAVOI	AFLLLVAGNA	(242)
2	---	epgd	DL	SALISvqddd		-dg-----	rL	SADELTSI	ALVLLLAGFE	(243)
3	---	cpkd	VM	SLLANskld		--gn-----	yi	DDKYINAY	YVAIATAGHD	(254)
4	---	kpgt	DAI	SIVANGqvn		--gr-----	pi	TSDEAKRM	CGLLLVGGED	(251)
5	---	geqs	DL	THMLNgkdpe	t-ge-----		pl	DDENIRYQ	IITFLIAGHE	(267)
6	---	v-nnpr	DEI	DCFLIkmeqe	n---n---l		ef	TLESIVIA	VSDLFGAGTE	(279)
7	---	v-nnpr	DEI	DCFLIkmeqe	n---n---l		ef	TLESIVIA	VSDLFGAGTE	(297)
8	---	ptdksdr	DL	DVLIA-vkae	t-gt-----	p	rf	SADEITGM	FISMMFAGHH	(259)
9	---	svqkhrv	DFL	QLMMNahnds	kdkesh---		al	SDMEITAQ	SIIFIFAGYE	
10	---	dtqkhrv	DFL	QLMIDshkns	keteshk---		al	SDLELVAQ	SIIFIFAGYE	
11	---	dtqkhrv	DFL	QLMIDsq-ns	keteshk---		al	SDLELVAQ	SIIFIFAGYE	(307)
12	---	dkqkhrv	DFL	QLMIDsq-ns	keteshk---		al	SDLELVAQ	SIIFIFAGYE	
13	---	dkqkhrv	DFL	QOMIDsq-ns	ketkshk---		al	SDLELVAQ	SIIFIFAGYE	
14	---	dkqkrrv	DFL	QLMINSq-ns	keidshk---		al	DDIEVVAQ	SIIFIFAGYE	
15	---	etqkhrv	DFL	QLMIDsq-ns	kdsethk---		al	SDLELVAQ	SIIFIFAGYE	(308)
16	---	dkqkhrv	DFL	QLMINSq-ns	kemdthk---		al	SDLELVAQ	SIIFIFAGYE	
17	---	dqqkrrv	DFL	QLMINSq-ns	kemdphk---		sl	SNEELVAQ	GIIFIFAGYE	
18	---	nkekqr	DFL	QLMINSq-ny	ktkeshk---		al	SDVEIVAQ	SVIFIFAGYE	

CSB 6

CSB 7A

1	TMVNMI	ALGV	ATIAQ	HEDQ	LAOLKA	----	----	np	SLA	(272)
2	ASVSL	IGIGT	YLAET	HEDQ	LALVRA	----	----	dp	SAL	(273)
3	TSSSS	SGGAT	IGISR	NEEO	LALAKS	----	----	dp	ALI	(284)
4	TVNPF	ESFSM	EFIAK	SEEH	ROELIE	----	----	rp	ERI	(281)
5	TSGLS	SFAL	YEVK	NEHV	LOKAAE	-aa	rv	lvdp-vps	ykqv	(314)
6	TSTTR	YSYL	LLILK	HEEV	AARVOE	er	vi	grhrs-pc	mqdr	(327)
7	TSTTR	YSYL	LLILK	HEEV	AARVOE	er	vi	grhrs-pc	mqdr	(345)
8	TSSGT	ASWTL	IEEMR	HRDA	YAAVIDE	-ld	ely	gdgrsvs	fhair	(307)
9	PSTST	SFVL	HSEAT	HEDT	QOKLOE	dr	alp	nka-ppt	ydtv	
10	TSSSV	SFIM	YSEAT	HEDV	QOKLOE	da	vl	pka-ppt	ydtv	
11	TSSSV	SFIM	YSEAT	HEDV	QOKLOE	da	vl	pka-ppt	ydtv	(355)
12	TSSSV	SFIM	YSEAT	HEDV	QOKLOE	da	vl	pka-ppt	ydtv	
13	TSTST	PFIM	YSEAT	HEDV	QOKLOE	da	vl	pka-pvt	ydav	
14	TSTST	SFIM	HLSEAT	HEDV	QOKLOE	dt	ll	pke-lat	ydtl	
15	TSSSV	SFIM	YSEAT	HEDV	QOKLOE	da	vl	pka-ppt	ydtv	(356)
16	TSTST	SFLM	YSEAT	HEDV	QOKLOE	da	tf	pka-lpt	ydav	
17	TSSA	SLLA	YSEAT	HEDV	QOKLOE	da	tf	pka-ppt	ydav	
18	TSSA	SFAL	YLAET	HEDV	QOKLOE	da	alp	nka-pat	ydtl	

CSB 7A

CSB 7B

CSB 8

1	POFVE	ELCRY	HTAS	alai	KR	TAKEDVMIGD	-KLVR	ANEGI	IASNQSANRD	(321)
2	PNAVE	ELRY	IAPP	et	tTR	FAAEVEIGG	-VAI	POYSTV	LVANGAANRD	(321)
3	PRVDE	AVRW	TAPV	ks	fMR	TALADTEVRG	-ONIK	RGDRI	MLSYPSANRD	(332)
4	PAACE	ELLRR	FSLV	a--	dGR	ILTSDYEFHG	-VOL	KGDQI	LLPOMLSGLD	(328)
5	GMVLE	ALRL	WPTA	p	afSL	YAKEDTVLGG	eYPL	KGDEL	MVLIPQLHRD	(363)
6	DAVIE	IQRF	IDLL	ptnl	PH	AVTRDVRFRN	-YFI	PKGTDI	ITSLSVLHD	(376)
7	DAVIE	IQRF	IDLL	ptnl	PH	AVTRDVRFRN	-YFI	PKGTDI	ITSLSVLHD	(394)
8	ENVLE	TLRL	HPPL	i-	ILMR	VARGEFEVOG	-HRI	EGOLV	AASPAISNRI	(355)
9	DMVNE	TLRL	YPIG	nr	-LER	VCKKDVEING	-VF	PKGSV	MIPSYALHRD	
10	DMVNE	TLRL	FPIA	mr	-LER	VCKKDVEING	-MF	PKGVV	MIPSYALHRD	
11	DMVNE	TLRL	FPIA	mr	-LER	VCKKDVEING	-MF	PKGVV	MIPSYALHRD	(403)
12	DMVNE	TLRL	FFVA	ir	-LER	TCKKDVEING	-VF	PKGSV	MIPSYALHRD	
13	DMVNE	TLRL	FFV	sr	-VTR	VCKKDVEING	-VF	PKGLAV	MVPIYALHRD	
14	DMVNE	TLRL	YPIA	gr	-LER	VCKKDVEING	-TF	PKGTIV	MMPTYALHRD	
15	DMVNE	TLRL	FFVA	mr	-LER	VCKKDVEING	-MF	PKGVV	MIPSYALHRD	(404)
16	DMVNE	TLRL	YPIA	gr	-LER	VCKKDVEING	-VF	PKGTIV	MVPTFTLHRD	
17	DMVNE	TLRL	YPIA	ar	-LER	ACKKDVEING	-VF	PKGTIV	VVPFVLHRD	
18	DMVNE	TLRL	YPIA	gr	-LER	VCKKDVEING	-LF	PKGTIV	MIPFTALHRD	

CSB 8

CSB 9

CSB 10

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1	EEVE-ENEDE	ENMrk----	---wppq-dp	LGEGFGDHRG	LAEHLAKAEL	(362)
2	PSQF-PDEHR	EDVtrd----	---tr--gh	LSFGQGIHFC	MGRPLAKLEG	(360)
3	EEVE-SNEDE	EDitr-----	---p-n-rh	LGEGWGAHMC	LGQHLAKLEM	(371)
4	EREN-ACEMH	VDEsrq----	---k-v-sh	TPEGHGSHLC	LGQHLARRET	(367)
5	KTIW-DDVEE	ERerfenps	a--ipqh-ab	KPGNGORAC	IGQOPALHEA	(410)
6	EKAL-PNEKV	EDghfldes	-gnfkksdyF	MPSAGKRM	VSEGLARMEL	(424)
7	EKAF-PNEKV	EDghfldes	-gnfkksdyF	MPSAGKRM	VSEGLARMEL	(442)
8	PEDE-PDEHD	EVaryeqpr	qedllnrwtW	TPEGGRHRC	VGAALFIMOJ	(404)
9	PQHW-PEEEE	ERerfsken	kgsidpy-vY	LPEGNGPENC	IGMRFILNM	
10	PKYW-TEBEK	ELerfskkn	kdnippy-iY	TPEGSGPENC	IGMRFILNM	
11	PKYW-TEBEK	ELerfskkn	kdnidpy-iY	TPEGSGPENC	IGMRFILNM	(451)
12	PKYW-TEEEE	ERerfskk-	kdsidpy-iY	TPEGTPENC	IGMRFILNM	
13	PKYW-TEBEK	ELerfskkn	kdsidly-rY	IPGAGPENC	IGMRFILTN	
14	PQHW-TEDE	ERerfskkn	kdninpy-iY	HPGAGPENC	IGMRFILNI	
15	PKYW-TEBEK	ELerfskkn	kdnidpy-iY	TPEGSGPENC	IGMRFILNM	(452)
16	QSLW-PEEEE	ERerfsrkn	kdsinpy-tY	LPEGTPENC	IGMRFILNM	
17	PDLW-PEEEE	ERerfskkn	kdsinpy-mY	LPEGTPENC	IGMRFILNM	
18	PKYW-PEEEE	ERerfskkn	qdsinpy-mY	LPEGSGPENC	IGMRFILNM	
CSB 10 CSB 11		CSB 12A		CSB 12B		

1	TTVFSTLYOK	---PDLKVav	plgKINTPL NRdVGIVDLP	Vif	(403)
2	EVAERALEGR	Ep-ALSLGid	ad-DVVWRSS	LLLRGIDHLP	Vrldg (403)
3	KIFFEELLPK	L-kSVELsg	---PPRLVAT	NEVGGPKNV	Irftka (412)
4	IVTEKEWLTR	IpDFSIAE	g--AOIQHKS	GIVSGVOALP	Lvwdpattka v (414)
5	TLVCGMLKH	---DFEDHT	-n-YELDIKE	TLTLKPEGEV	Vkakskkipl ggip (459)
6	FLFITSILON	---KLQSLve	pkdLDITAVV	NGFVSVPPIY	Qlcf---ipi hhhh (473)
7	FLFITSILON	---KLQSLve	pkdLDITAVV	NGFVSVPPIY	Qlcf---ipi (487)
8	KAIFSIVLRE	Y---EFEMAqp	p-eSYRNDS	KMvVOLAQPA	Gvryrrrtgv (450)
9	KLATTKVLON	---SFKPCKe	tq-IPLKLSR	QGILQPTKPI	Ilkvvpr---
10	KLATIRVLON	---SFKPCKe	tq-IPLKLSL	GGILQPEKPI	Vlkvesr---
11	KLATIRVLON	---SFKPCKe	tq-IPLKLSL	GGILQPEKPI	Vlkvesrdgt vsga (502)
12	KLALIRVLON	---SFKPCKe	tq-IPLKLDT	QGILQPEKPI	Vlkvsrdgt lsge
13	KLAVIRVLON	---SFKPCKe	tq-IPLKLDN	LPILQPEKPI	Vlkvhldgi tsqp
14	KLALIRVLON	---SFKPCKe	tq-IPLKLDN	LPILQPEKPI	Vlkvhldgi tsqp
15	KLALIRVLON	---SFKPCKe	tq-IPLKLDN	LPILQPEKPI	Vlkvhldgi tsqp
16	KLALIRVLON	---SFKPCKe	tq-IPLKLDN	LPILQPEKPI	Vlkvhldgi tsqp
17	KLALIRVLON	---SFKPCKe	tq-IPLKLDN	LPILQPEKPI	Vlkvhldgi tsqp
18	KVALIRVLON	---TVQPCke	te-IPLKLSK	QGILQPENPL	Ilkvvsrdet vsde
CSB 12B		CSB 13*		CSB 13** CSB 13	

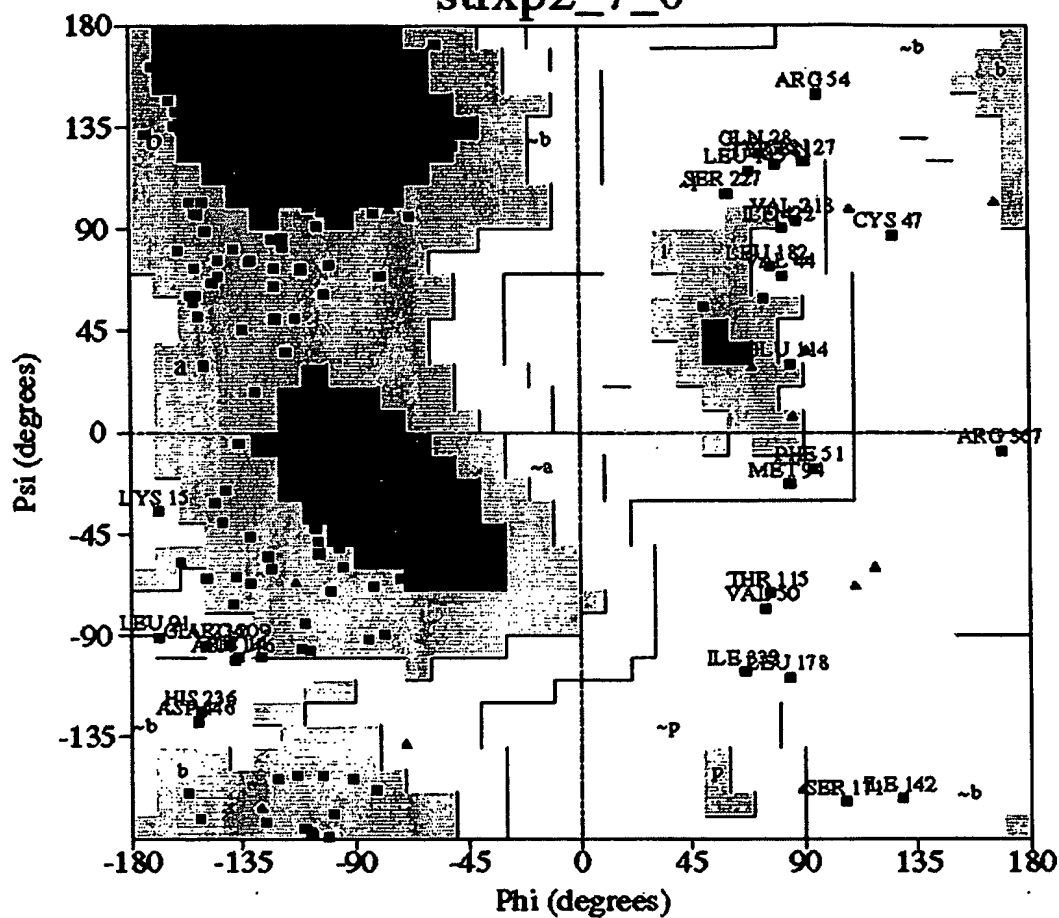
FIGURE 1

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PROCHECK

Ramachandran Plot

strxp2_7_0



Plot statistics

Residues in most favoured regions [A,B,L]	291	72.9%
Residues in additional allowed regions [a,b,l,p]	79	19.8%
Residues in generously allowed regions [-a,-b,-l,-p]	20	5.0%
Residues in disallowed regions	9	2.3%
Number of non-glycine and non-proline residues	399	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	21	
Number of proline residues	30	
Total number of residues	452	

FIGURE 2

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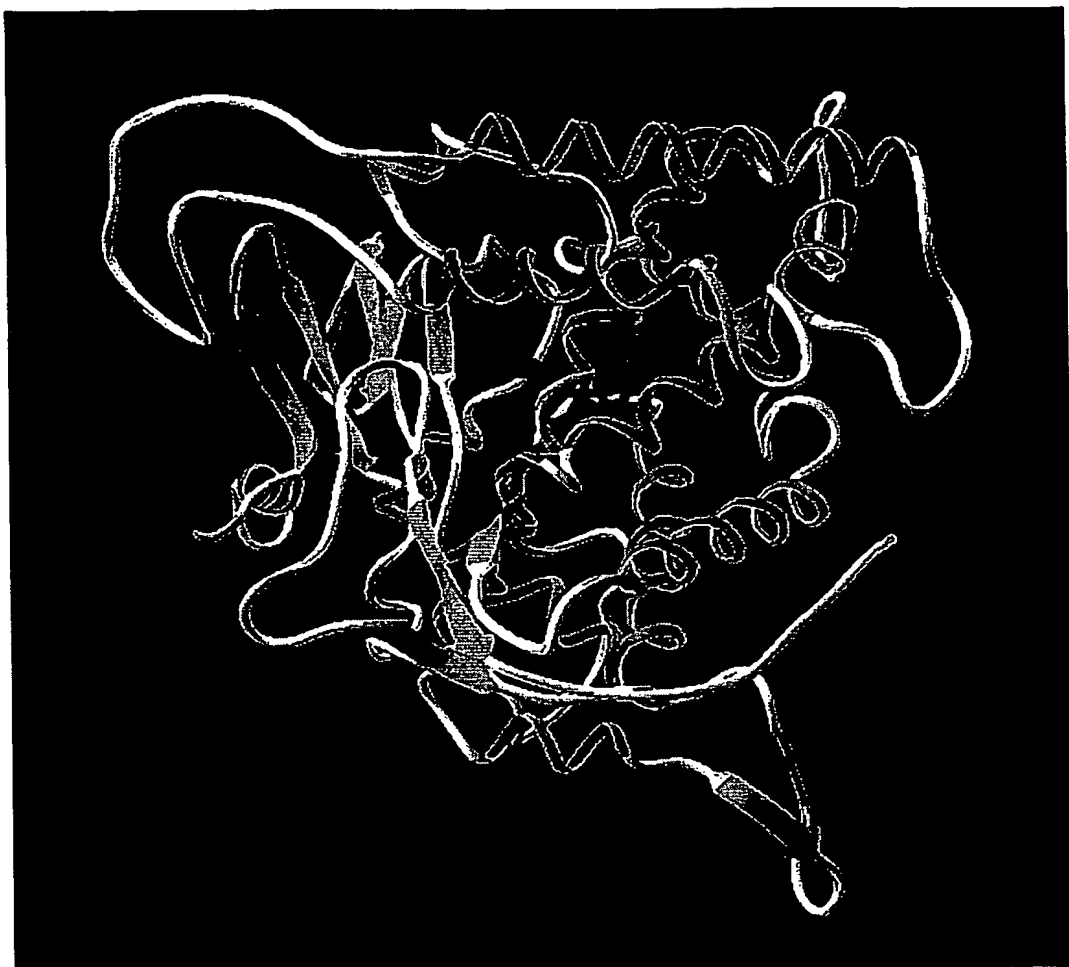


FIGURE 3

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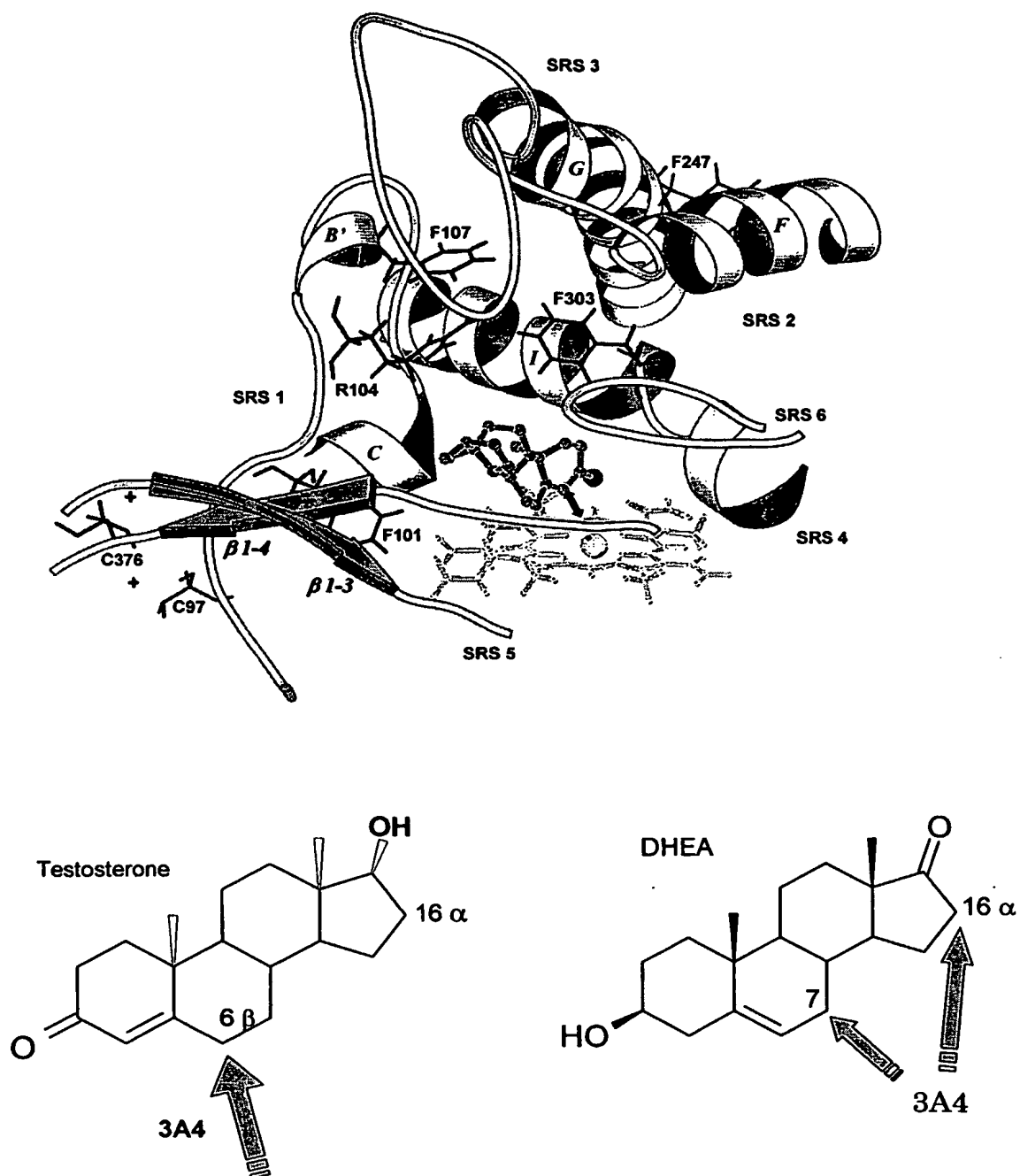


FIGURE 4A

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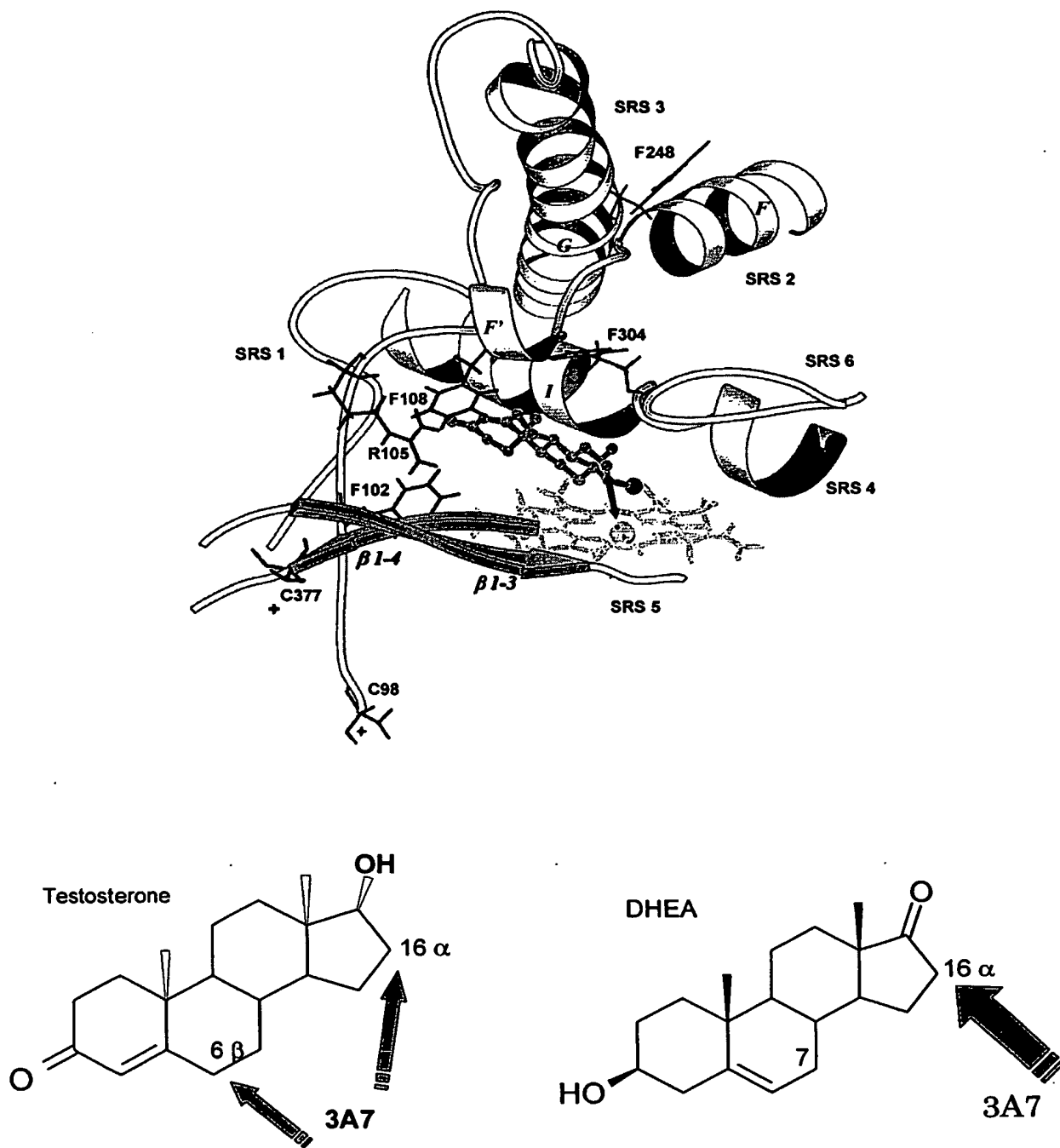


FIGURE 4B

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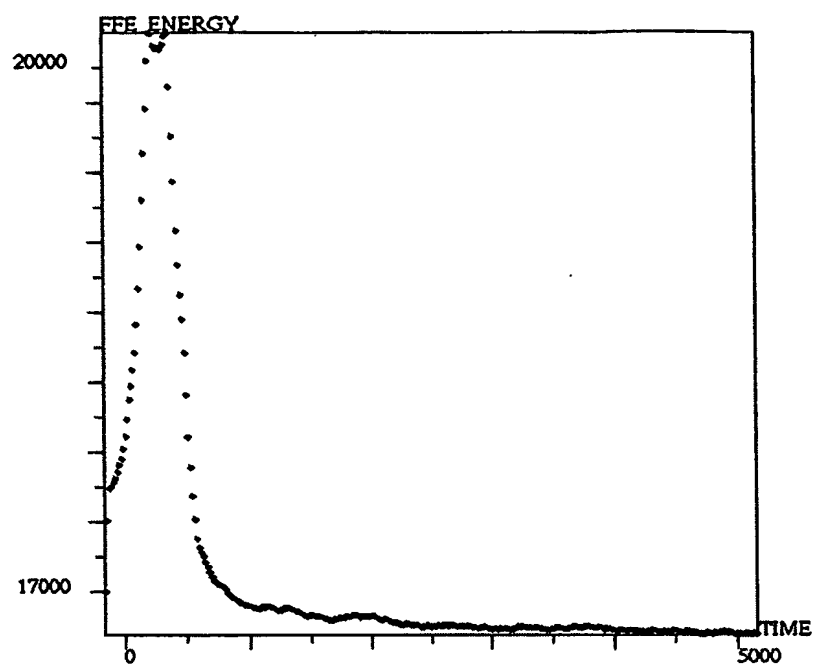


FIGURE 5